1652

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TECH CENTER 1600/2900

1600

#19

P.6

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/656,640A

DATE: 09/19/2002

TIME: 17:28:29

Input Set : A:\GC584-2-SEQLIST.TXT

Output Set: N:\CRF3\09192002\I656640A.raw

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 4 <110> APPLICANT: Wang, Huaming
 5        van Gastel, Frans
 6        Aehle, Wolfgang
 7        Rodrigues, Ana
 8        Topozada, Amr
10 <120> TITLE OF INVENTION: Phenol Oxidizing Enzyme Variants
13 <130> FILE REFERENCE: GC584-2
15 <140> CURRENT APPLICATION NUMBER: US 09/656,640A
16 <141> CURRENT FILING DATE: 2000-09-07
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 1958
24 <212> TYPE: DNA
25 <213> ORGANISM: Stachybotrys chartarum
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30  ctcaccaaga ggcagacgca gctgagtcct cccctggcct tgtacgaagt gcctctgccg     180
31  atccctcctc tgaaggcgcc caagtagtaa gtacattcta taggctagca gagccaacgt     240
32  tgctaatcat tgcagtaccg tccccaaccc caacactgga gaggacatct tgtactacga     300
33  gatggagatt aggcccttct cccaccagat ctacctgat ctggagccgg ccaacatggt      360
34  tggatacgat ggcatgtccc caggacctac catcatcgtt cctcgtggca ctgagagtgt     420
35  tgtccgcttc gtgaacagcg gagagaacac ctctcccaac agcgtccact tgcacggctc     480
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37  ggattactac taccccaaca ggcaggctgc ccgcatgctt tggtaccatg accatgccat     600
38  gtccatcacc gccgagaacg cctacatggg tcaggctggt gtctacatga tccaggaccc     660
39  ggctgaggat gccctgaacc tccccagcgg ctacggcgag tttgatatcc ccttggttct     720
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42  aagtatcgat gtatgaaatt gtgcatgctc taaccagtgc tatcacagaa cggtcagcct     900
43  tggcctatgc tcaacgtgca gccgcgcaag taccgcttcc gcttcctcaa cgctgccgtc     960
44  tcacgctctt tcgctctgta tcttgctacc tctgaggatt cagagaccag acttcccttc    1020
45  caggtcattg ccgctgacgg tggtctgctt gagggccctg ttgacactga cactctgtac    1080
46  atctctatgg ccgagcgctg ggaggttgtt atcgacttct ccaccttcgc tggccagtcc    1140
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48  actgacaagg tcatgcgatt cgtcgttgat gaagtccttg agtcgcccga cacttctgag    1260
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53  gacttccgag tcctttctcg ttccactgcc cgtggagtcg agccttatga ggctgctggt    1560
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/656,640A

DATE: 09/19/2002
TIME: 17:28:29

Input Set : A:\GC584-2-SEQLIST.TXT
Output Set: N:\CRF3\09192002\I656640A.raw

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57 ctttcaatgt cactgttctc ggtgactatg gctacaacta caccgagttc attgacccca    1800
58 tggagcctct ctggaggccc cgccccttcc tcctcggaga gttcgagaat ggctcgggtg    1860
59 acttcagcga gcttgccatc actgaccgca ttcaggagat ggctagcttc aacccctacg    1920
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63 <211> LENGTH: 583
64 <212> TYPE: PRT
65 <213> ORGANISM: Stachybotrys chartarum
67 <400> SEQUENCE: 2

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71               20                  25                  30
72 Met Pro Ser Gly Leu Thr Lys Arg Gln Thr Gln Leu Ser Pro Pro Leu
73           35                  40                  45
74 Ala Leu Tyr Glu Val Pro Leu Pro Ile Pro Pro Leu Lys Ala Pro Asn
75       50                  55                  60
76 Thr Val Pro Asn Pro Asn Thr Gly Glu Asp Ile Leu Tyr Tyr Glu Met
77 65                  70                  75                  80
78 Glu Ile Arg Pro Phe Ser His Gln Ile Tyr Pro Asp Leu Glu Pro Ala
79               85                  90                  95
80 Asn Met Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Ile Ile Val
81               100                 105                 110
82 Pro Arg Gly Thr Glu Ser Val Val Arg Phe Val Asn Ser Gly Glu Asn
83           115                 120                 125
84 Thr Ser Pro Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Pro
85       130                 135                 140
86 Phe Asp Gly Trp Ala Glu Asp Thr Thr Gln Pro Gly Glu Tyr Lys Asp
87 145                 150                 155                 160
88 Tyr Tyr Tyr Pro Asn Arg Gln Ala Ala Arg Met Leu Trp Tyr His Asp
89               165                 170                 175
90 His Ala Met Ser Ile Thr Ala Glu Asn Ala Tyr Met Gly Gln Ala Gly
91               180                 185                 190
92 Val Tyr Met Ile Gln Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser
93           195                 200                 205
94 Gly Tyr Gly Glu Phe Asp Ile Pro Leu Val Leu Thr Ala Lys Arg Tyr
95       210                 215                 220
96 Asn Ala Asp Gly Thr Leu Phe Ser Thr Asn Gly Glu Val Ser Ser Phe
97 225                 230                 235                 240
98 Trp Gly Asp Val Ile Gln Val Asn Gly Gln Pro Trp Pro Met Leu Asn
99               245                 250                 255
100 Val Gln Pro Arg Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser
101               260                 265                 270
102 Arg Ser Phe Ala Leu Tyr Leu Ala Thr Ser Glu Asp Ser Glu Thr Arg
103           275                 280                 285
104 Leu Pro Phe Gln Val Ile Ala Ala Asp Gly Gly Leu Leu Glu Gly Pro
105       290                 295                 300
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110 Leu Pro Gly Ala Asp Gly Leu Gly Val Glu Pro Glu Phe Asp Asn Thr
111                 340                 345                 350
112 Asp Lys Val Met Arg Phe Val Val Asp Glu Val Leu Glu Ser Pro Asp
113             355                 360                 365
114 Thr Ser Glu Val Pro Ala Asn Leu Arg Asp Val Pro Phe Pro Glu Gly
115     370                 375                 380
116 Gly Asn Trp Asp Pro Ala Asn Pro Thr Asp Asp Glu Thr Phe Thr Phe
117 385                 390                 395                 400
118 Gly Arg Ala Asn Gly Gln Trp Thr Ile Asn Gly Val Thr Phe Ser Asp
119                 405                 410                 415
120 Val Glu Asn Arg Leu Leu Arg Asn Val Pro Arg Asp Thr Val Glu Ile
121                 420                 425                 430
122 Trp Arg Leu Glu Asn Asn Ser Asn Gly Trp Thr His Pro Val His Ile
123         435                 440                 445
124 His Leu Val Asp Phe Arg Val Leu Ser Arg Ser Thr Ala Arg Gly Val
125     450                 455                 460
126 Glu Pro Tyr Glu Ala Ala Gly Leu Lys Asp Val Val Trp Leu Ala Arg
127 465                 470                 475                 480
128 Arg Glu Val Val Tyr Val Glu Ala His Tyr Ala Pro Phe Pro Gly Val
129                 485                 490                 495
130 Tyr Met Leu His Cys His Asn Leu Ile His Glu Asp His Asp Met Met
131             500                 505                 510
132 Ala Ala Phe Asn Val Thr Val Leu Gly Asp Tyr Gly Tyr Asn Tyr Thr
133         515                 520                 525
134 Glu Phe Ile Asp Pro Met Glu Pro Leu Trp Arg Pro Arg Pro Phe Leu
135     530                 535                 540
136 Leu Gly Glu Phe Glu Asn Gly Ser Gly Asp Phe Ser Glu Leu Ala Ile
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139                 565                 570                 575
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143 <210> SEQ ID NO: 3
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145 <212> TYPE: DNA
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151 gatcggcggc agctctgtcg atgccagatc cgttgctggt cgatcgacag acatgccttc      180
152 cggtctcacc aagaggcaga cgcagctgag tcctcccctg gccttgtacg aagtgcctct      240
153 gccgatccct cctctgaagg cgcccaagta gtaagtacat tctataggct agcagagcca      300
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159 acaaggatta ctactacccc aacaggcagg ctgcccgcat gctttggtac catgaccatg    660
160 ccatgtccat caccgccgag aacgcctaca tgggtcaggc tggtgtctac atgatccagg    720
161 acccggctga ggatgccctg aacctcccca gcggctacgg cgagtttgat atccccttgg    780
162 ttctgactgc caagcgatac aacgcagacg gcactctctt ctccaccaat ggagaggttt    840
163 ccagcttctg gggtgacgtt attcaagtgg taagttgagc ccattgagat gcttcagatc    900
164 ctagaagtat cgatgtatga aattgtgcat gctctaacca gtgctatcac agaacggtca  .  960
165 gccttggcct atgctcaacg tgcagccgcg caagtaccgc ttccgcttcc tcaacgctgc   1020
166 cgtctcacgc tctttcgctc tgtatcttgc tacctctgag gattcagaga ccagacttcc   1080
167 cttccaggtc attgccgctg acggtggtct gcttgagggc cctgttgaca ctgacactct   1140
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169 gtccatcgat atccgcaacc ttcctggtgc tgacggtctc ggtgttgagc ctgagtttga   1260
170 taacactgac aaggtcatgc gattcgtcgt tgatgaagtc cttgagtcgc ccgacacttc   1320
171 tgaggtgcct gccaacctcc gagatgttcc tttccccgag ggcggcaact gggaccccgc   1380
172 aaaccccact gatgacgaga ctttcacctt cggccgtgct aatggacagt ggacaatcaa   1440
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178 acaagtggtg tctacatgtt gcactgccac aacctgatcc acgaggacca cgacatgatg   1800
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180 cccatggagc ctctctggag gccccgcccc ttcctcctcg gagagttcga gaatggctcg   1920
181 ggtgacttca gcgagcttgc catcactgac cgcattcagg agatggctag cttcaacccc   1980
182 tacgcccagg ctgatgatga tgccgctgag gagtaaatat gatgatcgtc gaatgattta   2040
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186 <211> LENGTH: 572
187 <212> TYPE: PRT
188 <213> ORGANISM: Myrothecium verucaria
190 <400> SEQUENCE: 4
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194             20                  25                  30
195 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
196         35                  40                  45
197 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
198     50                  55                  60
199 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
200 65                  70                  75                  80
201 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
202             85                  90                  95
203 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
204             100                 105                 110
205 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
206         115                 120                 125
207 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
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213 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
214                   180                   185                   190
215 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
216             195                   200                   205
217 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
218       210                   215                   220
219 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
220 225                   230                   235                   240
221 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
222                   245                   250                   255
223 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
224             260                   265                   270
225 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
226             275                   280                   285
227 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
228       290                   295                   300
229 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
230 305                   310                   315                   320
231 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
232                   325                   330                   335
233 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
234             340                   345                   350
235 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser
236             355                   360                   365
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238       370                   375                   380
239 Asn Thr Pro Arg Gln Phe Arg Phe Gly Arg Thr Gly Pro Thr Trp Thr
240 385                   390                   395                   400
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243 Val Pro Val Gly Thr Val Glu Arg Trp Glu Leu Ile Asn Ala Gly Asn
244             420                   425                   430
245 Gly Trp Thr His Pro Ile His Ile His Leu Val Asp Phe Lys Val Ile
246             435                   440                   445
247 Ser Arg Thr Ser Gly Asn Asn Ala Arg Thr Val Met Pro Tyr Glu Ser
248       450                   455                   460
249 Gly Leu Lys Asp Val Val Trp Leu Gly Arg Arg Glu Thr Val Val Val
250 465                   470                   475                   480
251 Glu Ala His Tyr Ala Pro Phe Pro Gly Val Tyr Met Phe His Cys His
252             485                   490                   495
253 Asn Leu Ile His Glu Asp His Asp Met Met Ala Ala Phe Asn Ala Thr
254             500                   505                   510
255 Val Leu Pro Asp Tyr Gly Tyr Asn Ala Thr Val Phe Val Asp Pro Met
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/19/2002
PATENT APPLICATION: US/09/656,640A   TIME: 17:28:30

Input Set : A:\GC584-2-SEQLIST.TXT
Output Set: N:\CRF3\09192002\I656640A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 12
Seq#:8; N Pos. 12,18